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(FILE 'HOME' ENTERED AT 10:30:50 ON 10 SEP 2007)

FILE 'MEDLINE, EMBASE, BIOSIS' ENTERED AT 10:31:06 ON 10 SEP 2007

L1	1488 S ZCYTO18 OR MGC79382 OR (INTERLEUKIN (W) 21) OR (INTERLEUKIN
L2	1710 S L1 OR IL21 OR IL-21 OR IL-22
L3	118 S L2 (S) (CANCER OR INFLAMMATION OR ARTHRITIS)
L4	62 DUP REM L3 (56 DUPLICATES REMOVED)
L5	0 S L4 (S) GENETIC (S) ABNORMALITY
L6	0 S L4 (P) GENETIC (P) ABNORMALITY
L7	0 S L4 (P) 12Q15
L8	20 S L4 (P) (MRNA OR EXPRESSION)
L9	7 S L4 (S) (MRNA OR EXPRESSION)

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<!--StartFragment-->RESULT 6
US-09-870-574-1
; Sequence 1, Application US/09870574
; Patent No. 6551799
; GENERAL INFORMATION:
; APPLICANT: Gurney,Austin L.
; APPLICANT: Aggarwal,Sudeepta
; APPLICANT: Xie,Ming-Hong
; APPLICANT: Maruoka,Ellen M.
; APPLICANT: Foster,Jessica S.
; APPLICANT: Goddard,Audrey
; APPLICANT: Wood,William I.
; TITLE OF INVENTION: INTERLEUKIN-22 POLYPEPTIDES, NUCLEIC ACIDS ENCODING
; TITLE OF INVENTION: THE SAME AND METHODS FOR THE TREATMENT OF PANCREATIC DISORDERS
; FILE REFERENCE: P2806-1(US)
; CURRENT APPLICATION NUMBER: US/09/870,574
; CURRENT FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: US 60/169,495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 1
; LENGTH: 1152
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-870-574-1
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Query Match 99.8%; Score 1114; DB 3; Length 1152;
 Best Local Similarity 100.0%; Pred. No. 2.6e-266;
 Matches 1114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TCGAGTTAGAATTGTCTGCAATGGCCGCCCTGCAGAAATCTGTGAGCTCTTTCCTTATGG	60
Db	38	TCGAGTTAGAATTGTCTGCAATGGCCGCCCTGCAGAAATCTGTGAGCTCTTTCCTTATGG	97
Qy	61	GGACCCTGGCCACCAGCTGCCTCCTTCTCTTGGCCCTCTTGGTACAGGGAGGAGCAGCTG	120
Db	98	GGACCCTGGCCACCAGCTGCCTCCTTCTCTTGGCCCTCTTGGTACAGGGAGGAGCAGCTG	157
Qy	121	CGCCCATCAGCTCCCACTGCAGGCTTGACAAGTCCAACCTCCAGCAGCCCTATATCACCA	180
Db	158	CGCCCATCAGCTCCCACTGCAGGCTTGACAAGTCCAACCTCCAGCAGCCCTATATCACCA	217
Qy	181	ACCGCACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAACAACACAGACGTTTCGTC	240
Db	218	ACCGCACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAACAACACAGACGTTTCGTC	277
Qy	241	TCATTGGGGAGAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCTATCTGATGAAGC	300
Db	278	TCATTGGGGAGAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCTATCTGATGAAGC	337
Qy	301	AGGTGCTGAACTTCACCCCTGAAGAAGTGCTGTTCCCTCAATCTGATAGGTTCCAGCCTT	360
Db	338	AGGTGCTGAACTTCACCCCTGAAGAAGTGCTGTTCCCTCAATCTGATAGGTTCCAGCCTT	397
Qy	361	ATATGCAGGAGGTGGTGCCCTTCCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCATA	420
Db	398	ATATGCAGGAGGTGGTGCCCTTCCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCATA	457

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Qy      421 TTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAA 480
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Db      458 TTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAA 517

Qy      481 AGCTTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTTGCTGTTTATGTCTC 540
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Db      518 AGCTTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTTGCTGTTTATGTCTC 577

Qy      541 TGAGAAATGCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAATAACTAACCCCTTTCC 600
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Db      578 TGAGAAATGCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAATAACTAACCCCTTTCC 637

Qy      601 CTGCTAGAAAATAACAATTAGATGCCCCAAAGCGATTTTTTTTAACCAAAGGAAGATGGG 660
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Db      638 CTGCTAGAAAATAACAATTAGATGCCCCAAAGCGATTTTTTTTAACCAAAGGAAGATGGG 697

Qy      661 AAGCCAACTCCATCATGATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGA 720
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Qy      721 AACCAATGCCACTTTTGTGTTATAAGACCAGAAGGTAGACTTTCTAAGCATAGATATTTAT 780
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Db      758 AACCAATGCCACTTTTGTGTTATAAGACCAGAAGGTAGACTTTCTAAGCATAGATATTTAT 817

Qy      781 TGATAACATTTTCATTGTAAGTGGTGTCTATACACAGAAAACAATTTATTTTTTAAATAA 840
      |||
Db      818 TGATAACATTTTCATTGTAAGTGGTGTCTATACACAGAAAACAATTTATTTTTTAAATAA 877

Qy      841 TTGTCTTTTTCCATAAAAAAGATTACTTTCCATTCTTTAGGGGAAAAAACCCCTAAATA 900
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Db      878 TTGTCTTTTTCCATAAAAAAGATTACTTTCCATTCTTTAGGGGAAAAAACCCCTAAATA 937

Qy      901 GCTTCATGTTTCCATAATCAGTACTTTATATTTATAAATGTATTTATTATTATTATAAGA 960
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Db      938 GCTTCATGTTTCCATAATCAGTACTTTATATTTATAAATGTATTTATTATTATTATAAGA 997

Qy      961 CTGCATTTTATTTATATCATTTTATTAATATGGATTTATTTATAGAAACATCATTCGATA 1020
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Qy      1021 TTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTATAGAGCTATAACA 1080
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Db      1058 TTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTATAGAGCTATAACA 1117

Qy      1081 TGTTTATTTGACCTCAATAAACACTTGGATATCC 1114
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Db      1118 TGTTTATTTGACCTCAATAAACACTTGGATATCC 1151

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<!--EndFragment-->